181 4.1 162025 22 180.8 4.1 936 22 180.2 4.1 3334 16 177.8 4.1 35531 22	22 177.8 4.0 32174 22 AAR162906 Human breast or ov 24 177.8 4.0 32174 22 AAZ10752 Human genomic DNA 24 177.8 4.0 2459 22 AAZ4401 Human secreted produce of Human neuroblastom neuroblastom 177.2 4.0 12162 21 AAZ65349 Human neuroblastom 11ke produce of 30 177.2 4.0 9365 21 AAZ63359 Human CD39 11ke produce of 30 177.2 4.0 14747 2AAF63405 Human CD39 11ke produce pro	40 176.6 4.0 936 22 AAF58259 41 176.6 4.0 936 22 AAF58262 42 176.6 4.0 938 22 AAF58265 43 176.6 4.0 2406 22 AAH18479 44 176.2 4.0 168575 22 AAH121613 45 176.2 4.0 168575 22 AAH21613 ALIGNMENTS SULT 1 F50797/c AAH50797, AAH50797; 23-AUG-2001 (first entry) Human tumour associated cDNA #126. Human; cancer specific gene expression; gene therapy; age related differential expression; ss.	NOVEL NOVEL NOVEL SECTION 1000 SOUTH PROPERS INC. XX WOZ00136685-A2. XX T7-NOV-2000; 2000WO-US31809. PF 17-NOV-1999; 99US-0166056. PR 17-NOV-1999; 99US-0166106. XX Kroes RA, Moskal JR, Yamamoto H; XX WPI; 2001-355647/37. XX NOVEL nucleic acid molecules differentially expressed in brain cancers, PT useful for ascertaining propensity of cell for malignant phenotype or XX XX XX NOVEL nucleic acid molecules differentially expressed in brain cancers, PT useful for ascertaining suitability of anti-neoplastic drug candidate -
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. COM nucleic - nucleic search, using sw model Run on: March 15, 2002, 03:40:08; Search time 196.63 Seconds (without alignments) COUNTY 15, 2002, 03:40:08 (Without alignments) COUNTY 15, 2002, 03:40:08 (Without alignments) COUNTY 15, 2002, 03:40:08 (Without alignments)	Title: Perfect score: 4395 Sequence: 1 gaggggtccttgccaggccattatttgtaaaaaaaa 4395 Scoring table: IDENTITY_NUC Gapop 10.0, Gapext 1.0 Gapop 10.0, Gapext 1.0 Gapop 10.0, Gapext 1.0 Searched: 930621 seqs, 428662619 residues Total number of hits satisfying chosen parameters: 1861242 Minimum DB seq length: 200000000 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 100% Maximum Match 100% Listing first 45 summaries	N_Geneseq_1101:* SIDS2/gcgdata/geneseqn/NA1980.DAT:* SIDS2/gcgdata/geneseqn/NA1981.DAT:* SIDS2/gcgdata/geneseqn/NA1991.DAT:* SIDS2/gcgdata/geneseqn/NA1999.DAT:* SIDS2/gcgda	Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

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                                             cancers, particularly brain cancers such as haemangloblastoma, teratoma, haemangloma, glioblastoma, schwannoma, osteoma and pinealoma. The present sequence is a cancer-associated cDNA of the invention.
                               of the
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                                                                                                                                                                                                                                                                      Human; primer; detection; diagnosis; antisense therapy; gene therapy;
                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                 92
                      cDNA fragments
                  The present invention provides the sequences of 184 cDNA fragments are differentially expressed in cancer cell depending on the age opatient. They can be used to diagnose and identify treatments for
                                                                                                                                                                                                                                                                                                           Yamamoto J;
                                                                                                                                                                                             agatattotgtaagaatcaattggotatatggaatttaggataaagaatatttacaataa
                                                                                                                                                                                                                                                                                                                                                  3;
                                                                                                                  Score 317.4; DB 22; Length 385;
Pred. No. 5.6e-56;
0; Mismatches 6; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saito K, Ya
Otsuki T;
                                                                                      Sequence 385 BP; 127 A; 61 C; 43 G; 154 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nikawa T, Hayashi K, Sa
Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO:10637
Claim 28; Page 55; 82pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                     BP
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Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                    AAH13737 standard; cDNA; 1581
                                                                                                                Query Match 7.2%;
Best Local Similarity 97.5%;
Matches 344; Conservative
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11-JAN-2000; 2000JP-0118776.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cDNA sequence
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09-JUN-2000;
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The present invention describes primer sets for synthesising 5602
full-length cDNAs defined in the specification. Where a primer set
comprises: (a) an oligo-dT primer and an oligonucleotide comprises one of
the complementary strand of a polynucleotide which comprises one of
the 5602 nucleotide sequences defined in the specification, where the
coligonucleotide comprises at least 15 nucleotides; or (b) a combination
of an oligonucleotide comprises a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to a
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprises a 1'-end sequence (c)
sequence and an oligonucleotide comprises a 1'-end sequence, where the
coligonucleotide which comprises a 1'-end sequence, where the
coligonucleotide comprises at least 15 nucleotides and the combination of
the 5'-end sequence 13'-end sequence is selected from those defined in
the specification. The primers sets can be used in antisense therapy and
considerably. The primers are useful for synthesising polynucleotides,
particularly full-length cDNAs. The primers are also useful for the
detection and/cov diagnosis of the abnormality of the proteins encoded by
the full-length cDNAs. The primers allow obtaining of the full-length
connas easily without any specialised methods. AAH03166 to AAH13628 and
AAH13631 to AAH18742 represent human cDNA sequences; AAH03166 to AAH13628 and
AAH13631 to AAH18742 represent human cDNA sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               represent oligonucleotides, all of which are used in the exemplification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2395 tgcaacctccacttcctgggttcaagcgattctcctgcctcagcctcctaagtagctggg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1581;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 190.6; DB 22; Length Pred. No. 1e-29; 0; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G; 329 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human breast cancer associated 23172 coding sequence.
                                                                                                                       Claim 8; SEQ ID 10637; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1581 BP; 374 A; 439 C; 439
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ID AAF17845 standard; cDNA; 241
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Best Local Similarity 78.9%;
Matches 258; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the present invention.
                                                                                  full-length cDNAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                          primer; detection; diagnosis; antisense therapy; gene therapy;
                                                                                                                                                                                                                                                                          The present invention provides the coding sequences and some protein sequences of proteins associated with breast cancer in humans. These sequences can be used in the diagnosis and treatment of cancers,
 cancer associated gene; vaccine; diagnosis; therapy;
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                                                                                                                                                                                                                                                                                                                                                          4.3%; Score 189.2; DB 22; Length 241;
llarity 87.0%; Pred. No. 9.7e-30;
Conservative 0; Mismatches 30; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tacaataaagagtatttacaataaagagtttgttattatttgtaaaaaaa 4391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Harlocker SL;
                                                                                                                                                                                                                                                                                                                             Sequence 241 BP; 75 A; 24 C; 18 G; 112 T; 12 other
                                                                                                                                                                        Xu J,
                                                                                                                                                                                                              An isolated polypeptide useful for the tumors e.g. breast cancer comprises at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cDNA sequence SEQ ID NO:16686.
                                                                                                                                                                                                                                                        Claim 66; Page 189; 238pp; English.
                                                                                                                                                                        Mitcham JL,
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AAH17289/c
ID AAH17289 standard; CDNA; 3559
                                                                                                 99US-0285480.
99US-0339338.
99US-0389681.
99US-0433826.
                                                                                                                                                                                                                                                                                                          particularly breast tumours
                                                                              15-FEB-2000; 2000WO-US05308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-JUN-2001 (first entry
                                                                                                                                                                                                                                    breast tumor protein -
                                                                                                                                                                       Yuqiu J, Dillon DC,
                                                                                                                                                                                           WPI; 2001-122627/13.
                                                                                                                                                   (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 200; Conserv
                                       WO200060076-A2
breast
                     Homo sapiens
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                                                                                                                               03-NOV-1999;
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                                                                                                 02-APR-1999;
                                                                                                            23-JUN-1999;
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                                                           12-0CT-2000
                                                                                                                      02-SEP-1999
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 Human;
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Matches
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The present invention describes primer sets for synthesising 5602 (ull-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligounclectide complementary to the complementary strand of a polynuclectide which comprises one of the 5602 nucleotide sequences defined in the specification, where the cilisonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 3'-end sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence complementary to the coligonucleotide which comprises a 3'-end sequence (a) the 5'-end sequence of the complementary to a polynucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence is selected from those defined in the specification. The primers are used in antisense therapy and in specification. The primers are used in antisense therapy and particularly full-length cDNAs. The primers are used in the proteins encoded by the full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for AAH13628 and AAH13633 to AAH18642 represent human cDNA sequences; AAB92446 to AAH13622. AAB5683 represent human cDNA sequences; and AAH13629 to AAH13622.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       represent oligonucleotides, all of which are used in the exemplification
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                                                                                                                                                                                                                                                                                                 Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
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                                                                                                                                                                                                          Salto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.3%; Score 189.2; DB 22;
82.3%; Pred. No. 2.7e-29;
tive 0; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                               Claim 8; SEQ ID 16686; 2537pp + CD ROM; English.
                                                                                                                                                                                                                          Wakamatsu A, Nagai K,
                                                                                                                                                                                                      Hayash1
                                                                                                                                                                                                      Jta T, Isogai T, Nishikawa T,
Ishii S, Sugiyama T, Wakamatsu
                                                   29-JUL-1999; 99JP-0248036.
27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
                                                                                                                              2000JP-0241899
               2000EP-0116126
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nes 247; Conservative
                                                                                                                                                                   (HELI-) HELIX RES INST.
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                                                                                                                            000-JUN-2000;
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Matches
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02-0CT-2000;
02-0CT-2000;
13-0CT-2000;
13-0CT-2000;
                                                                                                                                                               Human; breast antigen; ovarian antigen; cancer; metastasis; gene therapy;
                                                                                                                              Human breast or ovarian antigen genomic DNA SEQ ID NO: 300.
                                AAI62650 standard; DNA; 16225 BP
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                                                                                                 (first entry)
                                                                                                                                                                                                                                                WO200155324-A2
                                                                                                                                                                                                                  Homo sapiens.
                                                                                                 19-OCT-2001
                                                                 AA162650;
RESULT
AA162650
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Human; colorectal cancer; colorectal cancer antigen; gene therapy;
                 Human colorectal cancer antigen coding sequence SEQ ID NO: 193
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2000US-0233064.
2000US-0233065.
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2000US-0205515
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24-FEB-2000;
16-MAR-2000;
17-MAR-2000;
17-MAR-2000;
19-MAY-2000;
07-JUN-2000;
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18-AUG-2000;
22-AUG-2000;
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22-AUG-2000;
23-AUG-2000;
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                                                                                                        Homo sapiens
                                                                                                                                                                                          02-AUG-2001.
ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides the protein and coding sequences of a number of ovarian and breast antigens. These are shown in AAIG2467-AAIG5572 and AAW42240-AAW42345. The sequences can be used in the diagnosis, prevention and treatment of breast and ovarian cancers, and their metastasses. The present sequence is a genomic sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2327 tettateattititititigaggiggagieteatieigitgeeeagge------ 2376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acids and polypeptides, useful for diagnosing treating and/or preventing human diseases and disorders
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AAI57656 standard; DNA; 25423 BP.
                                                                                                                                                                                                                                                                                                                       Rosen CA, Barash SC, Ruben SM;
               2000US-0251030.
2000US-0251988.
2000US-025179.
2000US-0251479.
2000US-0251856.
2000US-0251868.
                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                  08-DEC-2000; 2000US-0251989, 08-DEC-2000; 2000US-0251990, 11-DEC-2000; 2000US-0254097, 05-JAN-2001; 2001US-0259678.
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Matches 247; Conservative
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2000US-0251989
                                  25-SEP-2000;
26-SEP-2000;
27-SEP-2000;
27-SEP-2000;
29-SEP-2000;
29-SEP-2000;
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20-CCT-2000;
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17 - NOV - 2000;
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17-NOV-2000;
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2;
                                                                                                                                                                                                                                   number of colorectal cancer antigens. These are shown in AAA157619 and AAM38569-AAM38641. These can be used in the diagnosis, prevention and treatment of cancer of the colon and/or rectum. The present sequence is a colorectal cancer antigen genomic sequence. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the colon and rectum including colorectal cancers and also for testing and detection e.g. diagnosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2374 gctgg-----cctgatcttggctcactgcaacctccacttcctgggttcaagcga 2423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention provides the protein and coding sequences of
                                                                                                                                                                                                                                                                                                                                                                                      4.2%; Score 183.4; DB 22; Length 25423;
81.5%; Pred. No. 8.6e-28;
Live 0; Mismatches 41; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human colorectal cancer antigen coding sequence SEQ ID NO: 194
                                                                                                                                                                                           Disclosure; SEQ ID NO: 193; 522pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                               Sequence 25423 BP; 5518 A; 6899 C; 6921 G; 6085 T; 0 other;
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ID AAI57657 standard; DNA; 25424
                                                                                CA, Barash SC, Ruben
                                                     (HUMA-) HUMAN GENOME SCI INC
08-DEC-2000; 2000US-0251990
                         05-JAN-2001; 2001US-0259678
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Matches 242; Conservative
                                                                                                          WPI; 2001-457727/49.
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            11-DEC-2000;
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2000US - 0229513
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2000US - 0231243
2000US - 0231243
2000US - 0231243
2000US - 0231413
2000US - 0231413
2000US - 0231968
2000US - 0231968
2000US - 0231968
2000US - 0231968
2000US - 0231397
2000US - 0231399
2000US - 02313993
2000US - 0231399
2000US - 0231393
2000US-0179065.
2000US-0184664.
2000US-0186350.
2000US-0189174.
2000US-0199173.
2000US-0205515.
2000US-0205515.
2000US-0205615.
2000US-0215135.
2000US-0216880.
2000US-0216880.
2000US-0218290.
2000US-0218290.
2000US-0218290.
2000US-0218290.
2000US-0218290.
2000US-0218290.
2000US-0218290.
2000US-0218290.
2000US-0228213.
2000US-0228518.
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2000US-0225268.
2000US-0225270.
2000US-0225747.
2000US-0225757.
2000US-0225758.
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2000US-0226681.
2000US-0226868.
2000US-0227182.
2000US-0227009.
2000US-0228924.
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06-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
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08-SEP-2000;
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02-OCT-2000; 2000US-0237037.
02-OCT-2000; 2000US-0237039.
02-OCT-2000; 2000US-0237039.
02-OCT-2000; 2000US-0237040.
13-OCT-2000; 2000US-023935.
13-OCT-2000; 2000US-023937.
20-OCT-2000; 2000US-023937.
20-OCT-2000; 2000US-0241785.
20-OCT-2000; 2000US-0241786.
20-OCT-2000; 2000US-0241826.
20-OCT-2000; 2000US-0246178.
20-OCT-2000; 2000US-0246178.
20-OCT-2000; 2000US-0246178.
20-OCT-2000; 2000US-0246178.
20-OCT-2000; 2000US-0246178.
20-OCT-2000; 2000US-0246211.
20-OCT-2000; 2000US-0249211.
20-DEC-2000; 2000US

Ruben SM; Barash SC, (HUMA-) HUMAN GENOME cy, Rosen

WPI; 2001-457727/49

Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the colon and rectum including colorectal cancers and also for testing and detection e.g. diagnosis $^{\circ}$

Fri Mar 15 14:21:15 2002

3

Gaps

16;

46; .8e-28;

DB 22; Length 700; Indels

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present invention provides the protein and
                                                              at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                              Query Match
Best Local Similarity 81.5%;
Matches 242; Conservative
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ID AAH92304 standard; DNA; 700
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                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                            WO200142511-A2
      Disclosure;
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The present invention describes a method for detecting the presence of polymorphisms associated with inflammatory bowel diseases such as ulcerative colitis and crohn's disease. The methods can be used to detect the presence of genetic polymorphisms associated with inflammatory bowel used in this way for phenotypic correlations, forensies, paternity testing, medicine and genetic analysis. The present sequence is a genetic containing a polymorphic site described in the exemplification of the
                                                                                                                                                                                                                                                                                                                                     2314 totottttttaotottatoattttttttttttgaggtggagtotoattotgttgoccag 2373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detection; diagnosis; antisense therapy; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                   2374 gc-----tggcctgatcttggctcactgcaacctccacttcctgggttcaagcga
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Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                          Score 181.8; DE
Pred. No. 4.8e-2
0; Mismatches
bowel disease, using a hybridization assay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cDNA clone (5'-primer) SEQ ID NO:794.
                               Disclosure; Page 177-178; 463pp; English.
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ID AAH03959 standard; cDNA; 883 BP.
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2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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                                                                                                                                                                                                                                                                                         Similarity
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11-JAN-2000;
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                                              number of colorectal cancer antigens. These are shown in AAIS7547-AAIS7619 and AAM38569-AAM38641. These can be used in the diagnosis, prevention and treatment of cancer of the colon and/or rectum. The present sequence is a colorectal cancer antigen genomic sequence. Note: The sequence data for this patent did not form part of the prined specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                    17837 TITATETETATETETATETETATETETETTTTGAGATGGAGTCTCGCTCTGTTGCCTAG 17778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis single nucleotide polymorphism; SNP; chromosome 19p13; paternity test; chromosome 5q31-33; forensic test; gene therapy; ds.
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                                             sednences of
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                                                                                                                                                                                                                                  22; Length 25424;
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   ID NO: 194; 522pp + Sequence Listing; English,
                                                                                                                                                                           Sequence 25424 BP; 5521 A; 6900 C; 6922 G; 6081 T; 0 other;
                                                                                                                                                                                                                                                                41; Indels
                                           coding
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Pred. No. 8.6e-28;
0; Mismatches 41
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Saito K, , Otsuki

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1398..1648
/*tag= b
/note= "human OPA promoter"
complement (1565..1815)
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2321..2512
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5377.,5513
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6798..7027
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3608..3787
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7403..7483
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7615..7784
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2649..2805
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                                         Key
    The present invention describes primer sets for synthesising 5602 (fill-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary comprises: (a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the comprises and an oligonucleotide comprises a 1'-end sequence. Where the oligonucleotide which comprises at least 15 nucleotides and the combination of the specification. The primer sets selected from those defined in the specification. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers are also useful for the class and AAH13633 represent human anino acid sequences; and AAH13632 to AAH13632 condition and conditions and seasily without any specialised methods. AAH3645 to AAH13632 conditions and conditions and anino acid sequences; and AAH13632 to AAH13632 conditions.
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                         Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        457 ACTITITGIATITITAGIAGAGGATGGGGTTTCACCACGTTGTTCAGGCTGGTCTTGAACT 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42; Indels 14; Gaps
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mental retardation; autism; depression; bipolar affective disorder;
hypothyroidism; OPA gene; neuropsychiatric disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.1%; Score 181.8; DB 22; Length 883; Similarity 81.1%; Pred. No. 5.2e-28; Conservative 0; Mismatches 42; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA sequence of the wild type human PCTG4 region of Xq13.
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 883 BP; 273 A; 155 C; 199 G; 255 T; 1 other;
                                                                                        claim 1; SEQ ID 794; 2537pp + CD ROM; English.
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                                                                                                                                                                                                                                                                                                                                                                                           the present invention.
WPI; 2001-318749/34.
                                                                 full-length cDNAs
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Best Local Simil
Matches 241; C
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/note= "human 83018351 /*tag= s	「こ _を なっ」	/note= "human 89799122 /*tag= u /number= 19	/note= "human 96069769 /*tag= v /number= 20	/note= "human 997310104 /*tag= w /number= 21	ED×.		/number= 23 /note= "human 1123511355 /*tag= 2	/number 24 /note "human 1175112065 /*tag aa	/number= 25 /note= "human 1231712492 /*tag= ab	/number	/note= "human 1418714258 /*tag= ad /number= 28		/note- human 1501415175 /*tag- af /number- 30	/note= "human 1548715598 /*tag= ag /number= 31		/note= "human 1699917109 /*tag= ai /number= 33	"human 17492 aj er=34	'human
exon	FT FT FT FT	FT exon FT	FT exon FT FT	FT exon FT FT	FT FT exon FT	FT FT ET	FT exon	FT exon	er FT exon	T exon	er exon	exon	exon	exon	exon	exon	exon	

42298 tttgtatttttagtagagacggggtttcaccatgttggccaggctggtcttgactcg 42357 77; Indels 14; Gaps ----tattttagcagagatggggtttcactgtgttggccaggctggtgaactcctg Query Match

4.1%; Score 181.8; DB 21; Length 54548;
Best Local Similarity 74.2%; Pred. No. 2.4e-27;
Matches 262; Conservative 0; Mismatches 77; Indels 14; /*tag= au /note= "probable NL-3 promoter" /number= 41 /note= "human OPA promoter" 23878..24018 /*tag= ar /number= 42 /note= "human OPA promoter" /4531..24612 /*tag= as /number= 43 /note= "human OPA promoter" 24823..25096 /number- 44 /note- "human OPA promoter" 26123..26275 17736..17897 /*tag= ak /number= 35 /*tag= aq *tag- at promoter exon exon exon exon exon exon exon exon exon 2488 ò q ò g ŏ đ ò

ВР

standard; DNA; 162025

35.

(first entry)

RESULT 11

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Database; polymorphism; SNP; human; genetic marker; disease; infection;
                                                                                                        Human AKAP10 gene SEQ ID NO:
                                                                                                                                                                                                                                                                              13-OCT-1999; 99US-0159176.
10-JUL-2000; 2000US-0217251.
10-JUL-2000; 2000US-0217658.
19-SEP-2000; 2000US-0663968.
                                                                                                                                                                                                                                                                                                                                                  (SEQU-) SEQUENOM INC
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                                                                                                                                                  drug response; ds
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Jurinke C;
                           AAH02339
                                                     AAH02339;
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Matches
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                                                                                                        human; genetic marker; disease; infection;
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                                                                                                                                                                                                                                                                                                                                                  Chiu
                                                                                                                                                                                                                                                                                                                                                                                                                 Producing a database for identifying polymorphic genetic markers, comprises obtaining data relating to members of a healthy population and entering the information into a database -
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Pred. No. 5.3e-27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Page 241-288; 304pp; English.
                                                                                                                                                                                                                                                                                                                                                  Van Den Boom D,
 ВР
                                                                              36
 DNA; 161425
                                                                              Human AKAP10 gene SEQ ID NO:
                                                                                                        Database; polymorphism; SNP;
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ilarity 81.6%;
Conservative (
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10-JUL-2000; 2000US-0217658.
19-SEP-2000; 2000US-0663968.
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                                                                                                                                                                                                                                                      99US-0159176
                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                      (SEQU-) SEQUENOM INC
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AAH02340 standard;
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Best Local Similarity
Matches 239; Conserv
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                                                                                                                        drug response;
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Chiu N;

He L,

Rod1 C,

Ping Y,

Van Den Boom D,

Koester H,

2000WO-US28413

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124108
                                                                                                                                                                                                      The present invention provides a database of human samples obtained from
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                                                                                                                                                                                                                           healthy individuals which can be used to identify polymorphic genetic markers. Data obtained for the database can be used to sort the samples by parameters such as age, sex and ethnicity. This is useful in linking markers with diseases, susceptibility to infection and drug responses. The present sequence was used in an assay to demonstrate the uses of the database of the invention.
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Producing a database for identifying polymorphic genetic markers, comprises obtaining data relating to members of a healthy population and entering the information into a database -
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Pred. No. 5.3e-27;
0; Mismatches 40;
                                                                                                                                    Example 3; Page 196-241; 304pp; English.
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Local Similarity 81.6%;
nes 239; Conservative
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us-09-652-292-1.rng

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                                     The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic
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                                                                                                                                                                                                                                                                                                                         Electron-transfer group; ETM; mismatch; genotyping; gene expression; ss.
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17-MAR-2000; 2000US-0190259
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4.1%; Score 180.8; I
Best Local Similarity 0.7%; Pred. No. 8.5e-;
Matches 5; Conservative 526; Mismatches
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                                                                    AAF58252 standard; DNA; 936
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17-MAR-2000; 2000US-0190259.
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                                                                                                                  (first entry)
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Electron-transfer group; ETM; mismatch; genotyping;

gene expression; ss

WO200107665-A2

Synthetic.

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                                                                                       DB 22;
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                                                 Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other
detection of nucleic acids, especially of and single-nucleotide polymorphisms, e.g. monitoring gene expression.
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                         233; Indels
Query Match 4.1%; Score 180.8; DB 22; Best Local Similarity 0.7%; Pred. No. 8.5e-28; Matches 5; Conservative 526; Mismatches 233;
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ВР.

AAF58257 standard; DNA; 936

AAF58257

(first entry)

24-APR-2001 AAF58257;

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Oligonucleotide D1954

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Nucleic acids containing electron-transfer group, useful as labels i hybridization assays, e.g. for genotyping, allowing repeat analyses a single surface

(CLIN-) CLINICAL MICRO SENSORS INC

WPI; 2001-159728/16

Umek RM;

17-MAR-2000; 2000US-0190259

99US-0145695

26-JUL-1999;

26-JUL-2000; 2000WO-US20476

Example 6; Page 127; 159pp; English.

The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.

Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;

177	300 ИНЙИМИСИМИНИНИНИМИНИНИНИНИНИНИНИНИНИНИНИНИН	241
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0y 42	4232 agttgtgtgcaacaaacataccetttatctctgtaaaatttatacacacaaaattaaca 4291	4291
	180	121
0y 42	4292 aaagattotgtaagaattaattggotatatggaatttaggatagaatattacaataaag 4351	4351
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